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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2009; month=1; day=22; hr=16; min=26; sec=44; ms=514;]

=====

Reviewer Comments:

<210> 56

<211> 17752

<212> DNA

<213> Phaeodactylum tricornutum, Physcomitrella patens

<210> 71

<211> 17061

<212> DNA

<213> Phaeodactylum tricornutum, Physcomitrella patens, Caenorhabditis
elegans

The above <213> responses for sequence id#'s 56 and 71 are both
invalid, only one organism response is allowed for this line.

<210> 100

<211> 25

<212> DNA

<213> unknown

<220>

<221> misc_feature

<222> (1)..(25)

<223> ACtrau-5'

<210> 103

<211> 22
<212> DNA
<213> unknown

<220>
<221> misc_feature
<222> (1)..(22)
<223> YES-HIS-5'

Please explain the above <223> responses for sequence id#s 100 and 103.
FYI, please do not use foreign language in U.S. applications. Please
correct the remaining sequences showing similar errors.

Application No: 10552013 Version No: 2.0

Input Set:

Output Set:

Started: 2009-01-07 16:25:11.916
Finished: 2009-01-07 16:25:23.759
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 843 ms
Total Warnings: 109
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (28)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)
W 402	Undefined organism found in <213> in SEQ ID (31)
W 402	Undefined organism found in <213> in SEQ ID (32)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (36)
W 402	Undefined organism found in <213> in SEQ ID (37)
W 213	Artificial or Unknown found in <213> in SEQ ID (52)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (52)
W 213	Artificial or Unknown found in <213> in SEQ ID (53)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (53)
W 213	Artificial or Unknown found in <213> in SEQ ID (54)

Input Set:

Output Set:

Started: 2009-01-07 16:25:11.916
Finished: 2009-01-07 16:25:23.759
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 843 ms
Total Warnings: 109
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (54)
W 213	Artificial or Unknown found in <213> in SEQ ID (55)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (55)
W 402	Undefined organism found in <213> in SEQ ID (56)
W 402	Undefined organism found in <213> in SEQ ID (57)
W 402	Undefined organism found in <213> in SEQ ID (58)
W 402	Undefined organism found in <213> in SEQ ID (59)
W 213	Artificial or Unknown found in <213> in SEQ ID (60)
W 213	Artificial or Unknown found in <213> in SEQ ID (61)
W 213	Artificial or Unknown found in <213> in SEQ ID (62)
W 213	Artificial or Unknown found in <213> in SEQ ID (63)
W 213	Artificial or Unknown found in <213> in SEQ ID (64)
W 213	Artificial or Unknown found in <213> in SEQ ID (65)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (65)
W 213	Artificial or Unknown found in <213> in SEQ ID (66)
W 213	Artificial or Unknown found in <213> in SEQ ID (67)
W 213	Artificial or Unknown found in <213> in SEQ ID (68)
W 402	Undefined organism found in <213> in SEQ ID (71)
W 402	Undefined organism found in <213> in SEQ ID (72) This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (75)

Input Set:

Output Set:

Started: 2009-01-07 16:25:11.916
Finished: 2009-01-07 16:25:23.759
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 843 ms
Total Warnings: 109
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
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W 213	Artificial or Unknown found in <213> in SEQ ID (76)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (76)
W 213	Artificial or Unknown found in <213> in SEQ ID (77)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (77)
W 213	Artificial or Unknown found in <213> in SEQ ID (78)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (78)
W 213	Artificial or Unknown found in <213> in SEQ ID (79)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (79)
W 213	Artificial or Unknown found in <213> in SEQ ID (80)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (80)
W 213	Artificial or Unknown found in <213> in SEQ ID (81) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (81)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (82)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (83)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (84)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (85)

Input Set:

Output Set:

Started: 2009-01-07 16:25:11.916
Finished: 2009-01-07 16:25:23.759
Elapsed: 0 hr(s) 0 min(s) 11 sec(s) 843 ms
Total Warnings: 109
Total Errors: 51
No. of SeqIDs Defined: 148
Actual SeqID Count: 148

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (86)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (87)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (88)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (89) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Renz, Andreas
 Sozer, Nursen
 Frentzen, Margit
 Bauer, Jorg
 Keith, Stobart
 Fraser, Thomas
 Lazarus, Colin M
 Qi, Baoxiu
 Abbadi, Amine
 Heinz, Ernst

<120> NOVEL PLANT ACYLTRANSFERASES SPECIFIC FOR LONG-CHAINED, MULTIPLY
 UNSATURATED FATTY ACIDS

<130> 13478-00002-US

<140> 10552013

<141> 2005-09-30

<150> PCT/EP2004/003224

<151> 2004-03-26

<150> DE103 14 759.4

<151> 2003-03-31

<150> DE103 48 996.7

<151> 2003-10-17

<160> 148

<170> PatentIn version 3.3

<210> 1

<211> 1047

<212> DNA

<213> Thraustochytrium

<220>

<221> CDS

<222> (38)..(952)

<223> LPAAT

<400> 1

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                                   1               5
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Ala Lys Thr Ala Val Gly Leu Leu Thr Leu Ala Pro Ala Arg Ile Val
               10               15               20
ttc ctc gtg act gtc ctg ggc acg tac ggg ctc acg gtc gcg gcc tgc      151
Phe Leu Val Thr Val Leu Gly Thr Tyr Gly Leu Thr Val Ala Ala Cys
               25               30               35
acg cga ctt ggc gtc ccg aaa agc ttc gtg ctg ggc ctg acg cgg tgc      199
  
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Thr Arg Leu Gly Val Pro Lys Ser Phe Val Leu Gly Leu Thr Arg Cys	
40 45 50	
gtc gcg cga ctc acg ctc tgg ggg ctt ggg ttc tac cac att gag gtc	247
Val Ala Arg Leu Thr Leu Trp Gly Leu Gly Phe Tyr His Ile Glu Val	
55 60 65 70	
tct tgc gac gcc caa ggc ctt cgg gag tgg ccg cgc gtg att gtc gcg	295
Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp Pro Arg Val Ile Val Ala	
75 80 85	
aac cac gtc tcg tac ctg gag atc ttg tac ttc atg tcg acc gtg cac	343
Asn His Val Ser Tyr Leu Glu Ile Leu Tyr Phe Met Ser Thr Val His	
90 95 100	
tgc ccg tct ttc gtc atg aag aag acc tgc ctc cga gtc ccg ctt gtc	391
Cys Pro Ser Phe Val Met Lys Lys Thr Cys Leu Arg Val Pro Leu Val	
105 110 115	
ggc tac att gcc atg gag ctg ggc ggt gtg att gtg gac cgc gag ggc	439
Gly Tyr Ile Ala Met Glu Leu Gly Gly Val Ile Val Asp Arg Glu Gly	
120 125 130	
ggc ggt caa agc gca tcg gcg atc att cgc gac cgc gtg cag gag cct	487
Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg Asp Arg Val Gln Glu Pro	
135 140 145 150	
cct cga gat tcg tcg agc gag aag cac cac gcg cag ccg ctt ctt gtg	535
Pro Arg Asp Ser Ser Ser Glu Lys His His Ala Gln Pro Leu Leu Val	
155 160 165	
ttc ccc gag ggg acc acc acc aat gga agc tgc ctg ctc caa ttc aag	583
Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser Cys Leu Leu Gln Phe Lys	
170 175 180	
acg gga gcc ttt cgt cct ggg gct ccg gtg ctt ccg gtc gtg ctt gag	631
Thr Gly Ala Phe Arg Pro Gly Ala Pro Val Leu Pro Val Val Leu Glu	
185 190 195	
ttt ccg att gac aaa gcg cgt ggt gac ttt tcc ccg gcg tac gaa tcg	679
Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe Ser Pro Ala Tyr Glu Ser	
200 205 210	
gtc cac acg cca gct cac ctc ctt cgc atg ctc gca caa tgg agg cac	727
Val His Thr Pro Ala His Leu Leu Arg Met Leu Ala Gln Trp Arg His	
215 220 225 230	
cgg ctt cgg gtg cgc tat ctt cct ctg tat gag ccc tct gcg gct gag	775
Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr Glu Pro Ser Ala Ala Glu	
235 240 245	
aag gtt gat gca gac ctt tat gcg cgg aac gtg cgc gac gaa atg gcg	823
Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn Val Arg Asp Glu Met Ala	
250 255 260	
cgc gcg ctc aag gta ccc act gtg gag cag tct tac cgc gac aag ctc	871
Arg Ala Leu Lys Val Pro Thr Val Glu Gln Ser Tyr Arg Asp Lys Leu	
265 270 275	
gtc tac cac gcg gat ctc atg ccg cac tac cag aag gcc ggc ccc gga	919
Val Tyr His Ala Asp Leu Met Pro His Tyr Gln Lys Ala Gly Pro Gly	
280 285 290	
gcg ctc tat ctg tac gtc cga cct gac ctc ttg tagcactcat ggcggtccca	972
Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu Leu	
295 300 305	
agcgggtccag caacgggaga ttaaacacg atttcttagc ctacaaaaaa aaaaaaaaaa	1032
aaaaaaaaaa aaaaaa	1047

<210> 2

<211> 305

<212> PRT

<213> Thraustochytrium

<400> 2

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          20          25          30
Leu Thr Val Ala Ala Cys Thr Arg Leu Gly Val Pro Lys Ser Phe Val
          35          40          45
Leu Gly Leu Thr Arg Cys Val Ala Arg Leu Thr Leu Trp Gly Leu Gly
          50          55          60
Phe Tyr His Ile Glu Val Ser Cys Asp Ala Gln Gly Leu Arg Glu Trp
65          70          75          80
Pro Arg Val Ile Val Ala Asn His Val Ser Tyr Leu Glu Ile Leu Tyr
          85          90          95
Phe Met Ser Thr Val His Cys Pro Ser Phe Val Met Lys Lys Thr Cys
          100          105          110
Leu Arg Val Pro Leu Val Gly Tyr Ile Ala Met Glu Leu Gly Gly Val
          115          120          125
Ile Val Asp Arg Glu Gly Gly Gln Ser Ala Ser Ala Ile Ile Arg
          130          135          140
Asp Arg Val Gln Glu Pro Pro Arg Asp Ser Ser Ser Glu Lys His His
145          150          155          160
Ala Gln Pro Leu Leu Val Phe Pro Glu Gly Thr Thr Thr Asn Gly Ser
          165          170          175
Cys Leu Leu Gln Phe Lys Thr Gly Ala Phe Arg Pro Gly Ala Pro Val
          180          185          190
Leu Pro Val Val Leu Glu Phe Pro Ile Asp Lys Ala Arg Gly Asp Phe
          195          200          205
Ser Pro Ala Tyr Glu Ser Val His Thr Pro Ala His Leu Leu Arg Met
          210          215          220
Leu Ala Gln Trp Arg His Arg Leu Arg Val Arg Tyr Leu Pro Leu Tyr
225          230          235          240
Glu Pro Ser Ala Ala Glu Lys Val Asp Ala Asp Leu Tyr Ala Arg Asn
          245          250          255
Val Arg Asp Glu Met Ala Arg Ala Leu Lys Val Pro Thr Val Glu Gln
          260          265          270
Ser Tyr Arg Asp Lys Leu Val Tyr His Ala Asp Leu Met Pro His Tyr
          275          280          285
Gln Lys Ala Gly Pro Gly Ala Leu Tyr Leu Tyr Val Arg Pro Asp Leu
          290          295          300
Leu
305
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<210> 3

<211> 1701

<212> DNA

<213> Physcomitrella patens

<220>

<221> misc_feature

<223> LPAAT

<400> 3

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aactgaaaac ttgttttaat tttttcttaa attgaaatc tgtgcctgaa agccaactct    180
aggtecatca taatgtagca atatgatcag aagcgctcaa atgtgtcgtg aaagtttgc    240
tttgcaattt tcttttgcgt ttaacctatt gattatgttg gaaccacaat acagacgctg    300
cttcacttca ttcttatggc aatgaatgtc gtgatgattc cggttaattt catcctacag    360
ggatatggat gttgtaaagg tgatttttgc aggtgataaa gtacctagg agaaccgtgt    420
gatggtcacg tgcaaccatc gtaccgaagt ggactggatg tacatttgga acttagcaat    480
tcggaaaggc aagattgggt actgcaagta tgcggtgaag aactcagtga aaaacttacc    540
cttgttttgt tgggcatttt acgtttttga gtttctgatg ctgcatagaa agtgggaagt    600
ggatgctccc gtcatacaga catacattga cagttttcaa gataaaagag atcctctctg    660
gctagtcgtg tttcctgaag gcacagattt ttcgtaaggc tgaagtacc atccatggct    720
ttgatgtata tctgcaatct tctctataat ctgcatttat tctctgttgt ttctctagca    780
agtaaatcat acttgcttaa tgtacttagc aatttgtcat tttgactta ttgtgatgta    840
aatgtgattg actactatga cagtgaagcg aaacgggaca cgggcaatgc aattggaaga    900
gagaaaggct atccggagct tgtcaatgtg ctccaacctc gcaactcgtg ctttgtgact    960
tgcctttctc aatcgcgctg ctctttggat gcagtttatg acctcactat agggtagaag   1020
aagcgggtgc cttgttcat caacaatgta ttcggaaccg atccatcgga agtgacatt   1080
cacattcgcc gaataccaat ttctgagatt cctcaatcag aagacgggat gacgcagtgg   1140
ctgtatgac tattttatca aaaggaccag atgttggcca gttttagtaa gacaggctct   1200
ttccctgaca gtggaattga agagagccct ttgaacatag tggaagggtg ttgcaatgtt   1260
gctctacacg tagtccttag cggttgggta ttctgggtgt tgtttcattc ggtttggttg   1320
aagctttatg tggccttcgc tagtttgcgt ctgcggttta gtacctattt tgattggaga   1380
cctaaaccgg tttactctag tctacgtact aaaagaaaaa tcgtgtaaaa taaattcggt   1440
agttgtaatt ggtttgttta ttcgattcc aaagctgagt ttaagggtga ggctcctctt   1500
taagctgatt tttgtatta attggctgct cccttgtttg tctgccgtaa attggcttta   1560
atacggttgt cttctgctga tgaacctcag tgcttcaaga cgatgtggcc ttttagcctt   1620
ctcctttacc catcttgacc agatgccaaa ctgcgaataa agcagatcaa taggtcgtgc   1680
ccccaaaaaa aaaaaaaaaa a                                     1701
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<210> 4

<211> 714

<212> DNA

<213> *Physcomitrella patens*

<220>

<221> CDS

<222> (1)..(714)

<223> LPAAT

<400> 4

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1           5           10           15
tct gtt gtt tct cta gca agt aaa tca tac ttg ctt aat gta ctt agc    96
Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser
20          25          30
aat ttg tca ttt ttg act tat tgt gat gta aat gtg att gac tac tat   144
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr
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35	40	45	
gac agt gaa gcg aaa cgg gac acg ggc aat gca att gga aga gag aaa			192
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys			
50	55	60	
ggc tat ccg gag ctt gtc aat gtg ctt caa cct cgc act cgt ggc ttt			240
Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe			
65	70	75	80
gtg act tgc ctt tct caa tcg cgc tgc tct ttg gat gca gtt tat gac			288
Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp			
85	90	95	
ctc act ata ggg tac aag aag cgg tgt ccc ttg ttc atc aac aat gta			336
Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val			
100	105	110	
ttc gga acc gat cca tcg gaa gtg cac att cac att cgc cga ata cca			384
Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro			
115	120	125	
att tct gag att cct caa tca gaa gac ggt atg acg cag tgg ctg tat			432
Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr			
130	135	140	
gat cta ttt tat caa aag gac cag atg ttg gcc agt ttt agt aag aca			480
Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr			
145	150	155	160
ggc tct ttc cct gac agt gga att gaa gag agc cct ttg aac ata gtg			528
Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val			
165	170	175	
gaa ggt gtt tgc aat gtt gct cta cac gta gtc ctt agc ggt tgg gta			576
Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val			
180	185	190	
ttc tgg tgc ttg ttt cat tcg gtt tgg ttg aag ctt tat gtg gct ttc			624
Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe			
195	200	205	
gct agt ttg ctg ctc gcg ttt agt acc tat ttt gat tgg aga cct aaa			672
Ala Ser Leu Leu Leu Ala Phe Ser Thr Tyr Phe Asp Trp Arg Pro Lys			
210	215	220	
ccg gtt tac tct agt cta cgt act aaa aga aaa atc gtg taa			714
Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val			
225	230	235	

<210> 5

<211> 237

<212> PRT

<213> *Physcomitrella patens*

<400> 5

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Ser Val Val Ser Leu Ala Ser Lys Ser Tyr Leu Leu Asn Val Leu Ser		
20	25	30
Asn Leu Ser Phe Leu Thr Tyr Cys Asp Val Asn Val Ile Asp Tyr Tyr		
35	40	45
Asp Ser Glu Ala Lys Arg Asp Thr Gly Asn Ala Ile Gly Arg Glu Lys		
50	55	60

Gly Tyr Pro Glu Leu Val Asn Val Leu Gln Pro Arg Thr Arg Gly Phe
 65 70 75 80
 Val Thr Cys Leu Ser Gln Ser Arg Cys Ser Leu Asp Ala Val Tyr Asp
 85 90 95
 Leu Thr Ile Gly Tyr Lys Lys Arg Cys Pro Leu Phe Ile Asn Asn Val
 100 105 110
 Phe Gly Thr Asp Pro Ser Glu Val His Ile His Ile Arg Arg Ile Pro
 115 120 125
 Ile Ser Glu Ile Pro Gln Ser Glu Asp Gly Met Thr Gln Trp Leu Tyr
 130 135 140
 Asp Leu Phe Tyr Gln Lys Asp Gln Met Leu Ala Ser Phe Ser Lys Thr
 145 150 155 160
 Gly Ser Phe Pro Asp Ser Gly Ile Glu Glu Ser Pro Leu Asn Ile Val
 165 170 175
 Glu Gly Val Cys Asn Val Ala Leu His Val Val Leu Ser Gly Trp Val
 180 185 190
 Phe Trp Cys Leu Phe His Ser Val Trp Leu Lys Leu Tyr Val Ala Phe
 195 200 205
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 210 215 220
 Pro Val Tyr Ser Ser Leu Arg Thr Lys Arg Lys Ile Val
 225 230 235

<210> 6

<211> 507

<212> DNA

<213> *Physcomitrella patens*

<220>

<221> misc_feature

<223> LPAAT

<400> 6

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acaatatgtg gtcccacgtc atgttggtcc cggagggcac taccaccaat ggcagagcaa	180
taatgcctt caaaacagga gcattttcgc ctggtctccc tgtgcagcca atggttatta	240
gataccctca caagtatgtc aacctctctt ggtgtgacca aggaggtccg ttggtcgttg	300
tgttgcagct gatgactcag ttcattcaacc acatggaggt tgaatatattg ccggtcatga	360
agccaactgt gagagagatg aaataccctc atgaattcgc aagtagagtt cgcagcgaga	420
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tggtgcaga aaagctcaaa cagcctt	507

<210> 7

<211> 1566

<212> DNA

<213> *Physcomitrella patens*

<220>

<221> CDS

<222> (1)..(1566)

<223> LPAAT

<400> 7

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1          5          10          15
ctc aac ggg ctc gaa acg cca cta ctg gct gaa ttt cct ctt ggc gaa      96
Leu Asn Gly Leu Glu Thr Pro Leu Leu Ala Glu Phe Pro Leu Gly Glu
          20          25          30
cgg cct aca ata ggg ccg gag gca cca gta aat ccc ttc cat gaa ccc      144
Arg Pro Thr Ile Gly Pro Glu Ala Pro Val Asn Pro Phe His Glu Pro
          35          40          45
gat ggt ggt tgg aag acc aac aac gag tgg aat tac ttt caa atg atg      192
Asp Gly Gly Trp Lys Thr Asn Asn Glu Trp Asn Tyr Phe Gln Met Met
          50          55          60
aaa tcc att ttg ctg att cca ctt ctt ctc gtt cgt cta gtg agc atg      240
Lys Ser Ile Leu Leu Ile Pro Leu Leu Leu Val Arg Leu Val Ser Met
65          70          75          80
ata aca atc gta gca ttt gga tat gtg tgg atc agg att tgt ctg atc      288
Ile Thr Ile Val Ala Phe Gly Tyr Val Trp Ile Arg Ile Cys Leu Ile
          85          90          95
ggc gtc aca gat ccc ttg ttt aag
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